

10/566606

1 IAP9 Rec'd PCT/PTO 31 JAN 2006

SEQUENCE LISTING

5 <110> Degussa AG

10 <120> Process for the preparation of L-threonine

15 <130> 030217BT

20 <160> 10

25 <170> PatentIn version 3.1

30 20 <210> 1
 <211> 993
 <212> DNA
 <213> Escherichia coli

35 25 <220>
 <221> CDS
 <222> (1)..(990)
 <223> rpos gene

40 30 <400> 1
 atg agt cag aat acg ctg aaa gtt cat gat tta aat gaa gat gcg gaa 48
 Met Ser Gln Asn Thr Leu Lys Val His Asp Leu Asn Glu Asp Ala Glu
 1 5 10 15

45 35 ttt gat gag aac gga gtt gag gtt ttt gac gaa aag gcc tta gta gaa 96
 Phe Asp Glu Asn Gly Val Glu Val Phe Asp Glu Lys Ala Leu Val Glu
 20 25 30

50 40 cag gaa ccc agt gat aac gat ttg gcc gaa gag gaa ctg tta tcg cag 144
 Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Leu Leu Ser Gln
 35 40 45

55 45 gga gcc aca cag cgt gtg ttg gac gcg act cag ctt tac ctt ggt gag 192
 Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu
 50 55 60

60 50 att ggt tat tca cca ctg tta acg gcc gaa gaa gtt tat ttt gcg 240
 Ile Gly Tyr Ser Pro Leu Leu Thr Ala Glu Glu Val Tyr Phe Ala
 65 70 75 80

65 55 cgt cgc gca ctg cgt gga gat gtc gcc tct cgc cgc cgg atg atc gag 288
 Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu
 85 90 95

70 60 agt aac ttg cgt ctg gtg gta aaa att gcc cgc cgt tat ggc aat cgt 336
 Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg
 100 105 110

	ggt ctg gcg ttg ctg gac ctt atc gaa gag ggc aac ctg ggg ctg atc Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile 115 120 125	384
5	cgc gcg gta gag aag ttt gac ccg gaa cgt ggt ttc cgc ttc tca aca Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr 130 135 140	432
10	tac gca acc tgg tgg att cgc cag acg att gaa cgg gcg att atg aac Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn 145 150 155 160	480
15	caa acc cgt act att cgt ttg ccg att cac atc gta aag gag ctg aac Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn 165 170 175	528
20	gtt tac ctg cga acc gca cgt gag ttg tcc cat aag ctg gac cat gaa Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu 180 185 190	576
25	cca agt gcg gaa gag atc gca gag caa ctg gat aag cca gtt gat gac Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp 195 200 205	624
30	gtc agc cgt atg ctt cgt ctt aac gag cgc att acc tcg gta gac acc Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr 210 215 220	672
35	ccg ctg ggt gat tcc gaa aaa gcg ttg ctg gac atc ctg gcc gat Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp 225 230 235 240	720
40	gaa aaa gag aac ggt ccg gaa gat acc acg caa gat gac gat atg aag Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys 245 250 255	768
45	cag agc atc gtc aaa tgg ctg ttc gag ctg aac gcc aaa cag cgt gaa Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu 260 265 270	816
50	gtg ctg gca cgt cga ttc ggt ttg ctg ggg tac gaa gcg gca aca ctg Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu 275 280 285	864
55	gaa gat gta ggt cgt gaa att ggc ctc acc cgt gaa cgt gtt cgc cag Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln 290 295 300	912
60	att cag gtt gaa ggc ctg cgc cgt ttg cgc gaa atc ctg caa acg cag Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln 305 310 315 320	960
	ggg ctg aat atc gaa gcg ctg ttc cgc gag taa Gly Leu Asn Ile Glu Ala Leu Phe Arg Glu 325 330	993
	<210> 2	
	<211> 330	
	<212> PRT	
	<213> Escherichia coli	

<400> 2
Met Ser Gln Asn Thr Leu Lys Val His Asp Leu Asn Glu Asp Ala Glu
1 5 10 15

5 Phe Asp Glu Asn Gly Val Glu Val Phe Asp Glu Lys Ala Leu Val Glu
20 25 30

Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Leu Leu Ser Gln
10 35 40 45

Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu
50 55 60

Ile Gly Tyr Ser Pro Leu Leu Thr Ala Glu Glu Val Tyr Phe Ala
15 65 70 75 80

Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu
85 90 95

Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg
20 100 105 110

Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile
25 115 120 125

Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr
130 135 140

Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn
30 145 150 155 160

Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn
165 170 175

Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu
35 180 185 190

Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp
40 195 200 205

Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr
210 215 220

Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp
45 225 230 235 240

Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys
245 250 255

Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu
50 260 265 270

Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu
55 275 280 285

Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln
290 295 300

Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln
60 305 310 315 320

<220>
 <221> tRNA
 <222> (1)..(75)
 <223> supE allele

5
 <400> 4
 tgggtatcg ccaagcgta aggcaccgga ttctaattcc ggcattccga ggttcgaatc 60

10 ctcgtacccc agcca 75

<210> 5
 <211> 1545
 <212> DNA
 15 <213> Escherichia coli

20 <220>
 <221> CDS
 <222> (1)..(1542)
 <223> ilvA gene

25 <400> 5
 atg gct gac tcg caa ccc ctg tcc ggt gct ccg gaa ggt gcc gaa tat 48
 Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr
 1 5 10 15

30 tta aga gca gtg ctg cgc gcg ccg gtt tac gag gcg gcg cag gtt acg 96
 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr
 20 25 30

35 ccg cta caa aaa atg gaa aaa ctg tcg tcg cgt ctt gat aac gtc att 144
 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
 35 40 45

40 ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc 192
 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
 50 55 60

45 ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac 240
 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
 65 70 75 80

50 ggc gtg atc act gct tct gcg ggt aac cac gcg cag ggc gtc gcg ttt 288
 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
 85 90 95

55 tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc 336
 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
 100 105 110

60 acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg 384
 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
 115 120 125

65 ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa 432
 Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
 130 135 140

70 ctg tca cag cag cag ggg ttc acc tgg gtg ccg ccg ttc gac cat ccg 480
 Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
 145 150 155 160

	atg gtg att gcc ggg caa ggc acg ctg gcg ctg gaa ctg ctc cag cag Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln 165 170 175	528
5	gac gcc cat ctc gac cgc gta ttt gtg cca gtc ggc ggc ggc ggt ctg Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Leu 180 185 190	576
10	gct gct ggc gtg gcg gtg ctg atc aaa caa ctg atg ccg caa atc aaa Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys 195 200 205	624
15	gtg atc gcc gta gaa gcg gaa gac tcc gcc tgc ctg aaa gca gcg ctg Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu 210 215 220	672
20	gat gcg ggt cat ccg gtt gat ctg ccg cgc gta ggg cta ttt gct gaa Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu 225 230 235 240	720
25	ggc gta gcg gta aaa cgc atc ggt gac gaa acc ttc cgt tta tgc cag Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln 245 250 255	768
30	gag tat ctc gac gac atc atc acc gtc gat agc gat gcg atc tgt gcg Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala 260 265 270	816
35	gcg atg aag gat tta ttc gaa gat gtg cgc gcg gtg gcg gaa ccc tct Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Glu Pro Ser 275 280 285	864
40	ggc gcg ctg gcg ctg gcg gga atg aaa tat atc gcc ctg cac aac Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn 290 295 300	912
45	att cgc ggc gaa cgg ctg gcg cat att ctt tcc ggt gcc aac gtg aac Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn 305 310 315 320	960
50	ttc cac ggc ctg cgc tac gtc tca gaa cgc tgc gaa ctg ggc gaa cag Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln 325 330 335	1008
55	cgt gaa gcg ttg ttg gcg gtg acc att ccg gaa gaa aaa ggc agc ttc Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe 340 345 350	1056
60	ctc aaa ttc tgc caa ctg ctt ggc ggg cgt tcg gtc acc gag ttc aac Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn 355 360 365	1104
	tac cgt ttt gcc gat gcc aaa aac gcc tgc atc ttt gtc ggt gtg cgc Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg 370 375 380	1152
	ctg agc cgc ggc ctc gaa gag cgc aaa gaa att ttg cag atg ctc aac Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn 385 390 395 400	1200

gac ggc ggc tac agc gtg gtt gat ctc tcc gac gac gaa atg gcg aag Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys 405 410 415	1248
5 cta cac gtg cgc tat atg gtc ggc gga cgt cca tcg cat ccg ttg cag Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln 420 425 430	1296
10 gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu 435 440 445	1344
15 cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His 450 455 460	1392
20 tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu 465 470 475 480	1440
25 ctt ggc gac cat gaa ccg gat ttc gaa acc cgg ctg aat gag ctg ggc Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly 485 490 495	1488
30 50 tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu 500 505 510	1536
30 gcg ggt tag Ala Gly	1545
35 <210> 6 <211> 514 <212> PRT <213> Escherichia coli	
40 <400> 6 Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr 1 5 10 15	
45 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr 20 25 30	
50 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile 35 40 45	
55 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg 50 55 60	
60 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His 65 70 75 80	
65 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe 85 90 95	
70 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala 100 105 110	
75 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Glu Val 115 120 125	

Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
 130 135 140

5 Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
 145 150 155 160

Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln
 165 170 175

10 Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Leu
 180 185 190

15 Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys
 195 200 205

Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu
 210 215 220

20 Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu
 225 230 235 240

Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln
 245 250 255

25 Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala
 260 265 270

Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Glu Pro Ser
 30 275 280 285

Gly Ala Leu Ala Leu Ala Gly Met Lys Tyr Ile Ala Leu His Asn
 290 295 300

35 Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn
 305 310 315 320

Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln
 325 330 335

40 Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe
 340 345 350

Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn
 45 355 360 365

Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg
 370 375 380

50 Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn
 385 390 395 400

Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys
 55 405 410 415

Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln
 420 425 430

Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu
 60 435 440 445

Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His
 450 455 460
 Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu
 5 465 470 475 480
 Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly
 485 490 495
 10 Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu
 500 505 510
 Ala Gly
 15
 <210> 7
 <211> 1545
 <212> DNA
 20 <213> Escherichia coli
 <220>
 <221> CDS
 <222> (1)..(1542)
 25 <223> ilvA allele
 <220>
 <221> mutation
 30 <222> (856)..(856)
 <223>
 <400> 7
 35 atg gct gac tcg caa ccc ctg tcc ggt gct ccg gaa ggt gcc gaa tat 48
 Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr
 1 5 10 15
 40 tta aga gca gtg ctg cgc gcg ccg gtt tac gag gcg gcg cag gtt acg 96
 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr
 20 25 30
 ccg cta caa aaa atg gaa aaa ctg tcg cgt ctt gat aac gtc att 144
 45 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
 35 40 45
 ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc 192
 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
 50 55 60
 50 ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac 240
 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
 65 70 75 80
 55 ggc gtg atc act gct tct gcg ggt aac cac gcg cag ggc gtc gcg ttt 288
 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
 85 90 95
 60 tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc 336
 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
 100 105 110

	acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val 115 120 125	384
5	ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu 130 135 140	432
10	ctg tca cag cag ggg ttc acc tgg gtg ccg ccg ttc gac cat ccg Leu Ser Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro 145 150 155 160	480
15	atg gtg att gcc ggg caa ggc acg ctg gcg ctg gaa ctg ctc cag cag Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln 165 170 175	528
20	gac gcc cat ctc gac cgc gta ttt gtg cca gtc ggc ggc ggt ctg Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Leu 180 185 190	576
25	gtg atc gcc gta gaa gcg gaa gac tcc gcc tgc ctg aaa gca gcg ctg Val Ile Ala Val Glu Ala Asp Ser Ala Cys Leu Lys Ala Ala Leu 210 215 220	672
30	gat gcg ggt cat ccg gtt gat ctg ccg cgc gta ggg cta ttt gct gaa Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu 225 230 235 240	720
35	ggc gta gcg gta aaa cgc atc ggt gac gaa acc ttc cgt tta tgc cag Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln 245 250 255	768
40	gag tat ctc gac gac atc atc acc gtc gat agc gat gcg atc tgt gcg Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala 260 265 270	816
45	gcg atg aag gat tta ttc gaa gat gtg cgc gcg gtg gcg aaa ccc tct Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Lys Pro Ser 275 280 285	864
50	ggc gcg ctg gcg ctg gcg gga atg aaa aaa tat atc gcc ctg cac aac Gly Ala Leu Ala Leu Ala Gly Met Lys Tyr Ile Ala Leu His Asn 290 295 300	912
55	att cgc ggc gaa cgg ctg gcg cat att ctt tcc ggt gcc aac gtg aac Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn 305 310 315 320	960
	tac gtc tca gaa cgc tgc gaa ctg ggc gaa cag Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln 325 330 335	1008
60	cgt gaa gcg ttg ttg gcg gtg acc att ccg gaa gaa aaa ggc agc ttc Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe 340 345 350	1056

ctc aaa ttc tgc caa ctg ctt ggc ggg cgt tcg gtc acc gag ttc aac Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn 355 360 365	1104
5 tac cgt ttt gcc gat gcc aaa aac gcc tgc atc ttt gtc ggt gtg cgc Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg 370 375 380	1152
10 ctg agc cgc ggc ctc gaa gag cgc aaa gaa att ttg cag atg ctc aac Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn 385 390 395 400	1200
15 gac ggc ggc tac agc gtg gtt gat ctc tcc gac gac gaa atg gcg aag Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys 405 410 415	1248
20 cta cac gtg cgc tat atg gtc ggc gga cgt cca tcg cat ccg ttg cag Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln 420 425 430	1296
25 gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg Glu Arg Leu Tyr Ser Phe Glu Pro Glu Ser Pro Gly Ala Leu Leu 435 440 445	1344
30 cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His 450 455 460	1392
35 tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu 465 470 475 480	1440
40 ctt ggc gac cat gaa ccg gat ttc gaa acc ccg ctg aat gag ctg ggc Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly 485 490 495	1488
45 tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu 500 505 510	1536
50 gcg ggt tag Ala Gly	1545
55 <210> 8 <211> 514 <212> PRT <213> Escherichia coli	
60 <400> 8 Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr 1 5 10 15	
65 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr 20 25 30	
70 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile 35 40 45	
75 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg 50 55 60	

Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
 65 70 75 80

5 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
 85 90 95

Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
 100 105 110

10 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
 115 120 125

Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
 15 130 135 140

Leu Ser Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
 145 150 155 160

20 Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln
 165 170 175

Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Leu
 25 180 185 190

Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys
 195 200 205

30 Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu
 210 215 220

Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu
 35 225 230 235 240

Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln
 245 250 255

40 Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala
 260 265 270

Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Lys Pro Ser
 275 280 285

45 Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn
 290 295 300

Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn
 50 305 310 315 320

Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln
 325 330 335

Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe
 55 340 345 350

Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn
 355 360 365

60 Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg
 370 375 380

Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn
 385 390 395 400

5 Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys
 405 410 415

Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln
 420 425 430

10 Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu
 435 440 445

Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His
 450 455 460

15 Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu
 465 470 475 480

20 Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly
 485 490 495

Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu
 500 505 510

25 Ala Gly

<210> 9

<211> 1548

30 <212> DNA

<213> Escherichia coli

<220>

35 <221> DNA

<222> (1)...(1548)

<223>

40 <220>

<221> CDS

<222> (527)...(952)

<223> yjgF orf

45 <400> 9

tcgcgatctg gtactgttaag gggaaataga gatgacacac gataataaat tgcagggttga 60

50 agcttattaaa cgcggcacgg taattgacca tatccccgcc cagatcggtt ttaagctgtt 120

gagtctgttc aagctgaccg aaacggatca ggcgcattcacc attggctctga acctgccttc 180

tggcgagatg ggccgcaaag atctgatcaa aatcgaaaat accttttga gtgaagatca 240

55 agtagatcaa ctggcattgt atgcgccgca agccacgggtt aaccgtatcg acaactatga 300

agtggtggtt aaatcgccgca caagtctgcc ggagcgcac gacaatgtgc tggctgtccc 360

60 gaacagcaac tgttatcagcc atgccgaacc ggttcatcc agctttgccg tgcgaaaacg 420

cgc当地atgat atcgcgctca aatgcaaata ctgtaaaaa gagtttccc ataatgtgg 480

	gctggccaat taattgcgt tggtataaaa agtctggctc cctata atg agc cag Met Ser Gln 1	535
5	act ttt tac cgc tgt aat aaa gga gaa atc atg agc aaa act atc gcg Thr Phe Tyr Arg Cys Asn Lys Gly Glu Ile Met Ser Lys Thr Ile Ala 5 10 15	583
10	acg gaa aat gca ccg gca gct atc ggt cct tac gta cag ggc gtt gat Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr Val Gln Gly Val Asp 20 25 30 35	631
15	ctg ggc aat atg atc atc acc tcc ggt cag atc ccg gta aat ccg aaa Leu Gly Asn Met Ile Ile Thr Ser Gly Gln Ile Pro Val Asn Pro Lys 40 45 50	679
20	acg ggc gaa gta ccg gca gac gtc gct gca cag gca cgt cag tcg ctg Thr Gly Glu Val Pro Ala Asp Val Ala Ala Gln Ala Arg Gln Ser Leu 55 60 65	727
25	gat aac gta aaa gcg atc gtc gaa gcc gct ggc ctg aaa gtg ggc gac Asp Asn Val Lys Ala Ile Val Glu Ala Ala Gly Leu Lys Val Gly Asp 70 75 80	775
30	atc gtt aaa act acc gtc ttt gta aaa gat ctg aac gac ttc gca acc Ile Val Lys Thr Val Phe Val Lys Asp Leu Asn Asp Phe Ala Thr 85 90 95	823
35	gta aac gcc act tac gaa gcc ttc ttc acc gaa cac aac gcc acc ttc Val Asn Ala Thr Tyr Glu Ala Phe Phe Thr Glu His Asn Ala Thr Phe 100 105 110 115	871
40	ccg gca cgt tct tgc gtt gaa gtt gcc cgt ctg ccg aaa gac gtg aag Pro Ala Arg Ser Cys Val Glu Val Ala Arg Leu Pro Lys Asp Val Lys 120 125 130	919
45	att gag atc gaa gcg atc gct gtt cgt cgc taa tcttgatgga aatccggct Ile Glu Ile Glu Ala Ile Ala Val Arg Arg 135 140	972
50	atcatgcccg gattaagtct gatgacaaac gcaaaatcgc ctgatgcgt acgcttatca ggcctacgtg attcctgcaa tttattgaat ttgttggccg gataaggcat ttacggcga tccggcatga acaaaaactca ctttgtctac aatctgaatc gggctatcg tgcccagttt atataccctg ccagaatcgc aaccagccac gggaaatagc ttaacggcag cgccctgtaat tgcagataac tggccagcgg taaaaacggc aatgcgatcc cgacaatcat cacgatcacf gtcatgatca ttaacggcca cgatgcacag ctctgaataa acggcacacg gcgggtgcgg atcatatgca caatcagcgt ttgcgacagt aagcccccca caaaccatcc cgactggAAC agcgtttgcg ttccggcgt gttggcatgg aataccacc acatcaggca aaacgtcaaa atatcgaaga tcgagctgat cggtccgaag aagatc	1032 1092 1152 1212 1272 1332 1392 1452 1512 1548
60		

<210> 10
<211> 141
<212> PRT
<213> Escherichia coli

5

<400> 10
Met Ser Gln Thr Phe Tyr Arg Cys Asn Lys Gly Glu Ile Met Ser Lys
1 5 10 15

10

Thr Ile Ala Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr Val Gln
20 25 30

15

Gly Val Asp Leu Gly Asn Met Ile Ile Thr Ser Gly Gln Ile Pro Val
35 40 45

Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Val Ala Ala Gln Ala Arg
50 55 60

20

Gln Ser Leu Asp Asn Val Lys Ala Ile Val Glu Ala Ala Gly Leu Lys
65 70 75 80

Val Gly Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu Asn Asp
85 90 95

25

Phe Ala Thr Val Asn Ala Thr Tyr Glu Ala Phe Phe Thr Glu His Asn
100 105 110

30

Ala Thr Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg Leu Pro Lys
115 120 125

Asp Val Lys Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
130 135 140